



OICE

RAW SEQUENCE LISTING

DATE: 06/06/2002

PATENT APPLICATION: US/10/016,283

TIME: 11:36:24

Input Set : N:\Crf3\RULE60\10016283.raw

Output Set: N:\CRF3\06062002\J016283.raw

1 <110> APPLICANT: Valenzuela et al., David M.
 2 <120> TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
 3 <130> FILE REFERENCE: REG195-B-PCT-US
 4 <140> CURRENT APPLICATION NUMBER: 10/016,283
 5 <141> CURRENT FILING DATE: 2001-11-30
 7 <150> PRIOR APPLICATION NUMBER: US/09/077,955A
 8 <151> PRIOR FILING DATE: 1998-09-10
 11 <150> PRIOR APPLICATION NUMBER: PCT/US96/20696
 12 <151> PRIOR FILING DATE: 1996-12-13
 14 <160> NUMBER OF SEQ ID NOS: 36
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 868
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Rattus sp.
 21 <400> SEQUENCE: 1
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 23 1 5 10 15
 24 Ala Phe Ser Gly Thr Glu Lys Leu Pro Lys Ala Pro Val Ile Thr Thr
 25 20 25 30
 26 Pro Leu Glu Thr Val Asp Ala Leu Val Glu Glu Val Ala Thr Phe Met
 27 35 40 45
 28 Cys Ala Val Glu Ser Tyr Pro Gln Pro Glu Ile Ser Trp Thr Arg Asn
 29 50 55 60
 30 Lys Ile Leu Ile Lys Leu Phe Asp Thr Arg Tyr Ser Ile Arg Glu Asn
 31 65 70 75 80
 32 Gly Gln Leu Leu Thr Ile Leu Ser Val Glu Asp Ser Asp Asp Gly Ile
 33 85 90 95
 34 Tyr Cys Cys Thr Ala Asn Asn Gly Val Gly Gly Ala Val Glu Ser Cys
 35 100 105 110
 36 Gly Ala Leu Gln Val Lys Met Lys Pro Lys Ile Thr Arg Pro Pro Ile
 37 115 120 125
 38 Asn Val Lys Ile Ile Glu Gly Leu Lys Ala Val Leu Pro Cys Thr Thr
 39 130 135 140
 40 Met Gly Asn Pro Lys Pro Ser Val Ser Trp Ile Lys Gly Asp Ser Ala
 41 145 150 155 160
 42 Leu Arg Glu Asn Ser Arg Ile Ala Val Leu Glu Ser Gly Ser Leu Arg
 43 165 170 175
 44 Ile His Asn Val Gln Lys Glu Asp Ala Gly Gln Tyr Arg Cys Val Ala
 45 180 185 190
 46 Lys Asn Ser Leu Gly Thr Ala Tyr Ser Lys Leu Val Lys Leu Glu Val
 47 195 200 205
 48 Glu Val Phe Ala Arg Ile Leu Arg Ala Pro Glu Ser His Asn Val Thr

ENTERED

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49	210	215	220
50	Phe Gly Ser Phe Val Thr Leu Arg Cys Thr Ala Ile Gly Met Pro Val		
51	225	230	235
52	Pro Thr Ile Ser Trp Ile Glu Asn Gly Asn Ala Val Ser Ser Gly Ser		240
53		245	250
54	Ile Gln Glu Asn Val Lys Asp Arg Val Ile Asp Ser Arg Leu Gln Leu		255
55		260	265
56	Phe Ile Thr Lys Pro Gly Leu Tyr Thr Cys Ile Ala Thr Asn Lys His		270
57		275	280
58	Gly Glu Lys Phe Ser Thr Ala Lys Ala Ala Thr Val Ser Ile Ala		285
59		290	295
60	Glu Trp Ser Lys Ser Gln Lys Glu Ser Lys Gly Tyr Cys Ala Gln Tyr		300
61	305	310	315
62	Arg Gly Glu Val Cys Asp Ala Val Leu Val Lys Asp Ser Leu Val Phe		320
63		325	330
64	Phe Asn Thr Ser Tyr Pro Asp Pro Glu Glu Ala Gln Glu Leu Leu Ile		335
65		340	345
66	His Thr Ala Trp Asn Glu Leu Lys Ala Val Ser Pro Leu Cys Arg Pro		350
67		355	360
68	Ala Ala Glu Ala Leu Leu Cys Asn His Leu Phe Gln Glu Cys Ser Pro		365
69		370	375
70	Gly Val Leu Pro Thr Pro Met Pro Ile Cys Arg Glu Tyr Cys Leu Ala		380
71	385	390	395
72	Val Lys Glu Leu Phe Cys Ala Lys Glu Trp Leu Ala Met Glu Gly Lys		400
73		405	410
74	Thr His Arg Gly Leu Tyr Arg Ser Gly Met His Phe Leu Pro Val Pro		415
75		420	425
76	Glu Cys Ser Lys Leu Pro Ser Met His Gln Asp Pro Thr Ala Cys Thr		430
77		435	440
78	Arg Leu Pro Tyr Leu Asp Tyr Lys Lys Glu Asn Ile Thr Thr Phe Pro		445
79		450	455
80	Ser Ile Thr Ser Ser Lys Pro Ser Val Asp Ile Pro Asn Leu Pro Ala		460
81	465	470	475
82	Ser Thr Ser Ser Phe Ala Val Ser Pro Ala Tyr Ser Met Thr Val Ile		480
83		485	490
84	Ile Ser Ile Met Ser Cys Phe Ala Val Phe Ala Leu Leu Thr Ile Thr		495
85		500	505
86	Thr Leu Tyr Cys Cys Arg Arg Arg Glu Trp Lys Asn Lys Lys Arg		510
87		515	520
88	Glu Ser Ala Ala Val Thr Leu Thr Thr Leu Pro Ser Glu Leu Leu Leu		525
89		530	535
90	Asp Arg Leu His Pro Asn Pro Met Tyr Gln Arg Met Pro Leu Leu Leu		540
91	545	550	555
92	Asn Pro Lys Leu Leu Ser Leu Glu Tyr Pro Arg Asn Asn Ile Glu Tyr		560
93		565	570
94	Val Arg Asp Ile Gly Glu Gly Ala Phe Gly Arg Val Phe Gln Ala Arg		575
95		580	585
96	Ala Pro Gly Leu Leu Pro Tyr Glu Pro Phe Thr Met Val Ala Val Lys		590
97		595	600
			605

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98      Met Leu Lys Glu Glu Ala Ser Ala Asp Met Gln Ala Asp Phe Gln Arg
99      610                      615                      620
100     Glu Ala Ala Leu Met Ala Glu Phe Asp Asn Pro Asn Ile Val Lys Leu
101     625                      630                      635                      640
102     Leu Gly Val Cys Ala Val Gly Lys Pro Met Cys Leu Leu Phe Glu Tyr
103     645                      650                      655
104     Met Ala Tyr Gly Asp Leu Asn Glu Phe Leu Arg Ser Met Ser Pro His
105     660                      665                      670
106     Thr Val Cys Ser Leu Ser His Ser Asp Leu Ser Thr Arg Ala Arg Val
107     675                      680                      685
108     Ser Ser Pro Gly Pro Pro Pro Leu Ser Cys Ala Glu Gln Leu Cys Ile
109     690                      695                      700
110     Ala Arg Gln Val Ala Ala Gly Met Ala Tyr Leu Ser Glu Arg Lys Phe
111     705                      710                      715                      720
112     Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Met
113     725                      730                      735
114     Val Val Lys Ile Ala Asp Phe Gly Leu Ser Arg Asn Ile Tyr Ser Ala
115     740                      745                      750
116     Asp Tyr Tyr Lys Ala Asp Gly Asn Asp Ala Ile Pro Ile Arg Trp Met
117     755                      760                      765
118     Pro Pro Glu Ser Ile Phe Tyr Asn Arg Tyr Thr Thr Glu Ser Asp Val
119     770                      775                      780
120     Trp Ala Tyr Gly Val Val Leu Trp Glu Ile Phe Ser Tyr Gly Leu Gln
121     785                      790                      795                      800
122     Pro Tyr Tyr Gly Met Ala His Glu Glu Val Ile Tyr Tyr Val Arg Asp
123     805                      810                      815
124     Gly Asn Ile Leu Ala Cys Pro Glu Asn Cys Pro Leu Glu Leu Tyr Asn
125     820                      825                      830
126     Leu Met Arg Leu Cys Trp Ser Lys Leu Pro Ala Asp Arg Pro Ser Phe
127     835                      840                      845
128     Cys Ser Ile His Arg Ile Leu Gln Arg Met Cys Glu Arg Ala Glu Gly
129     850                      855                      860
130     Thr Val Gly Val
131     865
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 2869
135 <212> TYPE: DNA
136 <213> ORGANISM: Rattus sp.
137 <220> FEATURE:
138 <221> NAME/KEY: modified_base
139 <222> LOCATION: (2817)
140 <223> OTHER INFORMATION: n=a, c, g, or t
141 <220> FEATURE:
142 <221> NAME/KEY: modified_base
143 <222> LOCATION: (2823)
144 <223> OTHER INFORMATION: n=a, c, g, or t
145 <220> FEATURE:
146 <221> NAME/KEY: modified_base
147 <222> LOCATION: (2824)

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148 <223> OTHER INFORMATION: n=a, c, g, or t
149 <220> FEATURE:
150 <221> NAME/KEY: modified_base
151 <222> LOCATION: (2867)
152 <223> OTHER INFORMATION: n=a, c, g, or t
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155   aatgtaaac cagggagcgt tttttttcct cacattgtcc agaagcaacc tttcttcctg 120
156   agcctggatt aatcatgaga gagctcgtca acattccact gttacagatg ctcaccctgg 180
157   ttgccttcag cgggaccgag aaacttccaa aagcccctgt catcaccacg cctcttgaaa 240
158   ctgtagatgc cttagttgaa gaagtggcga ctttcatgtg cgccgtggaa tcctaccctc 300
159   agcctgaaat ttcttgacc agaaataaaa ttctcatcaa gctgtttgac acccgctaca 360
160   gcatccgaga gaacggtcag ctctcacca tcctgagtggt ggaggacagt gatgatggca 420
161   tetaetgetg cacagccaac aatggagtggt gaggagcgggt ggaaagtgtt ggcgcctgc 480
162   aagtgaagat gaagcctaaa ataactcgtc ctcccatcaa tgtaaaaata attgagggat 540
163   tgaaagcagt cctaccgtgc actacgatgg gtaaccccaa gccatccgtg tcctggatta 600
164   agggggacag tgctctcagg gaaaattcca ggattgcagt tcttgaatct gggagttaa 660
165   ggatccataa tgtgcaaaaag gaagacgcag gacagtaacc atgtgtggca aaaaacagcc 720
166   tgggacacag ttactccaaa ctggtgaagc tggaagtggg ggtttttgca agaatacctg 780
167   gtgctcctga atcccacaat gtcacctttg gttcctttgt aaccctacgc tgcacagcaa 840
168   taggcatgcc tgtccccacc atcagctgga ttgaaaacgg aaatgctgtt tcttcagggt 900
169   ccattcaaga gaatgtgaaa gaccgagtga ttgactcaag actccagctc tttatcacaa 960
170   agccaggact ctacacatgc atagctacca ataagcatgg agagaaattc agtaccgcaa 1020
171   aggctgcagc cactgtcagt atagcagaat ggagcaaata acagaaagaa agcaaaaggct 1080
172   actgtgcca gtacagagg gaggtgtgtg atgccgtcct ggtgaaagac tctcttgtct 1140
173   tcttcaacac ctctatccc gacctgagg aggcccaaga gctgctgac cactgtcgt 1200
174   ggaatgaact caaggctgtg agcccactct gccgaccagc tgccgaggct ctgctgtgta 1260
175   atcacctctt ccaggagtgc agccctggag tgctacctac tcctatgccc atttgagag 1320
176   agtaactgctt ggcagtaaaag gagctcttct gtgcaaagga atggctggca atggaaggga 1380
177   agaccacccg cgactctac agatccggga tgcatctcct cccggtcccg gagtgcagca 1440
178   agcttcccag catgcaccag gacccacag cctgcacaag actgccgtat ttagattata 1500
179   aaaaagaaaa cataacaaca tcccgtcca taacgtcctc caagccgagc gtggacattc 1560
180   caaacctgcc tgcctccacg tcttccttcg ccgtctcgcc tgcgtactcc atgactgtca 1620
181   tcatctccat catgtcctgc tttgcggtgt ttgctctcct caccatcact actctctatt 1680
182   gctgccgaag gaggagagag tggaaaaata agaaaagaga gtcggcagcg gtgacctca 1740
183   ccacattgcc ttccgagctc ctgctggaca ggctgcatcc caaccccatg taccagagga 1800
184   tgccactcct tctgaatccc aagttgctca gcctggagta tccgaggaat aacatcgagt 1860
185   atgtcagaga catcgagag ggagcgtttg gaagggtctt tcaagcgagg gcccaggct 1920
186   tgcttcctta tgaaccttc actatggtgg ctgtgaagat gctgaaggag gaggcctccg 1980
187   cagatatgca ggcagacttt cagagggagg cagccctcat ggcggagtgt gacaaccca 2040
188   acattgtgaa gctcttaggt gtgtgtgtgt ttgggaagcc aatgtgcctg ctctttgaat 2100
189   atatggccta tggtagctc aatgagtcc tccgaagcat gtccctcac actgtgtgca 2160
190   gcctcagcca cagtgcctg tccacgagg ctccggtgtc cagccctggt cctccacccc 2220
191   tgtcttgtgc ggaacagctc tgtattgcca ggcaagtggc agctggcatg gcctacctgt 2280
192   cggagcgcaa gtttgtccat cgggacttag ctaccaggaa ctgcctggtt ggagagaaca 2340
193   tgggtggtgaa aattgcagac tttggcctct ctaggaaacat ctactccgca gactactaca 2400
194   aagctgatgg aaacgatgct atacctatcc gctggatgcc acccgagtct atcttctaca 2460
195   accgctacac cacggagtca gatgtgtggg cttatggcgt ggtcctctgg gagatcttct 2520
196   cctatggact gcagccctac tatggaatgg cccatgagga ggtcatttac tatgtgagag 2580

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197      atggtaacat ccttgccctgc cctgagaaact gtcccttgga actgtacaac cttatgcgcc 2640
198      tatgttgagg caagctgcct gcagacagac ccagcttctg cagtatccac cggatccctgc 2700
199      agcgcattgtg cgagagagca gagggaaacgg taggcgtcta aggttgacca tgctcaaaca 2760
W--> 200      acacccagga ggatcttttc agactgcgag ctggaggggat cctaaagcag agggcgnata 2820
W--> 201      agnncagata ggaagagttt atctcaggca gcacgtncag ttggttggtt      2869
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 6
205 <212> TYPE: PRT
206 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
209 <400> SEQUENCE: 3
210      Asp Val Trp Ala Tyr Gly
211      1              5
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214 <211> LENGTH: 29
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
219 <220> FEATURE:
220 <221> NAME/KEY: modified_base
221 <222> LOCATION: (18)
222 <223> OTHER INFORMATION: n=a, c, g, or t
223 <220> FEATURE:
224 <221> NAME/KEY: modified_base
225 <222> LOCATION: (24)
226 <223> OTHER INFORMATION: n=a, c, g, or t
227 <400> SEQUENCE: 4
W--> 228      gaattcgagc tcccrwangc ccanacrtc      29
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 6
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
236 <400> SEQUENCE: 5
237      Asp Leu Ala Thr Arg Asn
238      1              5
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 28
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
246 <220> FEATURE:
247 <221> NAME/KEY: modified_base
248 <222> LOCATION: (17)
249 <223> OTHER INFORMATION: n=a, c, g, or t

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 2817,2823,2824,2857

Seq#:4; N Pos. 18,24

Seq#:6; N Pos. 17,20,23,26

Seq#:8; N Pos. 17,20,23,26

Seq#:10; N Pos. 6,12

Seq#:12; N Pos. 6,12

Seq#:14; N Pos. 6,12,15

Seq#:15; N Pos. 18,24

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10016283.raw

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L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:2760
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:2820
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0